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BLAST Search Results

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BLASTP 2.1.1 [Aug-8-2000]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 972929850-514-6426

Query= SEQIDNO:X
(667 letters)

Database: nr
576,719 sequences; 181,542,687 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 13 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:		Score	E
		(bits)	Value
ref NP_060628.1	hypothetical protein FLJ10624 >gi 7022772 ...	1319	0.0
gb AAB88191.1	(AF035526) kanadaptin [Mus musculus]	768	0.0
gb AAF55582.1	(AE003723) CG7706 gene product [Drosophila m...	337	2e-91
sp P34648 YOT2 CAEEL	HYPOTHETICAL 80.5 KD PROTEIN ZK632.2 I...	293	5e-78
dbj BAB08640.1	(AB009048) gene_id:K15E6.5~unknown protein ...	189	6e-47
pir I51116	NF-180 - sea lamprey >gi 632549 gb AAA80106.1 ...	72	2e-11
gb AAF45312.1	(AE002936) CG17168 gene product [Drosophila ...	72	2e-11
dbj BAB11326.1	(AB016886) gene_id:MCA23.11~unknown protein...	69	1e-10
pir T25596	hypothetical protein C32E8.5 - Caenorhabditis e...	68	4e-10
sp Q28147 PPR8 BOVIN	NUCLEAR INHIBITOR OF PROTEIN PHOSPHATA...	66	1e-09

Alignments

>ref|NP_060628.1| hypothetical protein FLJ10624
dbj|BAA91718.1| (AK001486) unnamed protein product [Homo sapiens]
Length = 796

Score = 1319 bits (3375), Expect = 0.0
Identities = 649/654 (99%), Positives = 650/654 (99%)

Query: 1 MADILSQSETLASQDLGDFKKPALPVSPAARSKAPASSSSNPPEEVQKEGPTALQDSNSG 60
MADILSQSETLASQDLGDFKKPALPVSPAARSKAPASSSSNPPEEVQKEGPTALQDSNSG
Sbjct: 55 MADILSQSETLASQDLGDFKKPALPVSPAARSKAPASSSSNPPEEVQKEGPTALQDSNSG 114

Query: 61 EPDIPPPQPDGDFRSLQEEQSRPTTAVSSPGGPAPAPPYQEPWPWGGPATAPYSLET LKG 120
EPDIPPPQPDGDFRSLQEEQSRPTTAVSSPGGPAPAPPYQEPWPWGGPATAPYSLET LKG
Sbjct: 115 EPDIPPPQPDGDFRSLQEEQSRPTTAVSSPGGPAPAPPYQEPWPWGGPATAPYSLET LKG 174

Query: 121 GTILGTRSLKGTSYCLFGRLSGCDVCLHPSVSRYPHAVLQHRASGPDGECDSNGPGFYLY 180
GTILGTRSLKGTSYCLFGRLSGCDVCLHPSVSRYPHAVLQHRASGPDGECDSNGPGFYLY
Sbjct: 175 GTILGTRSLKGTSYCLFGRLSGCDVCLHPSVSRYPHAVLQHRASGPDGECDSNGPGFYLY 234

Query: 181 DLGSTHGTFLNKTRIPRTYCRVHVGHVVRFGGSTRLFILQGPEEDREAESSELTVTQLKE 240
DLGSTHGTFLNKTRIPRTYCRVHVGHVVRFGGSTRLFILQGPEEDREAESSELTVTQLKE
Sbjct: 235 DLGSTHGTFLNKTRIPRTYCRVHVGHVVRFGGSTRLFILQGPEEDREAESSELTVTQLKE 294

Query: 241 LRKQQQIILLXKKMLGEDSDEEEEMDTSERKINAGSQDDEMGTWGMGEDAVEDDAEENPI 300
LRKQQQIILLXKKMLGEDSDEEEEMDTSERKINAGSQDDEMGTWGMGEDAVEDDAEENPI
Sbjct: 295 LRKQQQIILLXKKMLGEDSDEEEEMDTSERKINAGSQDDEMGTWGMGEDAVEDDAEENPI 354

Query: 301 VLEFQQEREAFYIKDPKKALQGFFDREGEELEYEFDEQGHSTWLCRVRLPVDDSTGKQLV 360
VLEFQQEREAFYIKDPKKALQGFFDREGEELEYEFDEQGHSTWLCRVRLPVDDSTGKQLV
Sbjct: 355 VLEFQQEREAFYIKDPKKALQGFFDREGEELEYEFDEQGHSTWLCRVRLPVDDSTGKQLV 414

Query: 361 AEAIHSGKKKEAMIQCSLEACRILDTLGLLRQEA VSRKRKAKNWEDEDFYDSDDDTFLDR 420
AEAIHSGKKKEAMIQCSLEACRILDTLGLLRQEA VSRKRKAKNWEDEDFYDSDDDTFLDR
Sbjct: 415 AEAIHSGKKKEAMIQCSLEACRILDTLGLLRQEA VSRKRKAKNWEDEDFYDSDDDTFLDR 474

Query: 421 TGLIEKKRLNRMKKAGKIDKPEFESLVAKLND AERELSEISERLKASSQVLSESPSQD 480
TGLIEKKRLNRMKKAGKIDKPEFESLVAKLND AERELSEISERLKASSQVLSESPSQD
Sbjct: 475 TGLIEKKRLNRMKKAGKIDKPEFESLVAKLND AERELSEISERLKASSQVLSESPSQD 534

Query: 481 SLDAFMSEMKGSTLDGVSRRKKLHLRTFELRKEQQRLKGLIKIVKPAEIPELKKTETQTT 540
SLDAFMSEMKGSTLDGVSRRKKLHLRTFELRKEQQRLKGLIKIVKPAEIPELKKTETQTT
Sbjct: 535 SLDAFMSEMKGSTLDGVSRRKKLHLRTFELRKEQQRLKGLIKIVKPAEIPELKKTETQTT 594

Query: 541 GAENKAKKLTLPFLGAMKGGSKFKLKTGTVGKLPKRPELPPTLMRMKDEPEVEEEEEEE 600
GAENKAKKLTLPFLGAMKGGSKFKLKTGTVGKLPKRPELPPTLMRMKDEPEVEEEEEEE
Sbjct: 595 GAENKAKKLTLPFLGAMKGGSKFKLKTGTVGKLPKRPELPPTLMRMKDEPEVEEEEEEE 654

Query: 601 EEEEEKEEHEKKKKLEDGSLSRPQPEIEPEAAVQEMRPPTDLTHFKETQTHGNI 654
EEEEKEKEEHEKKKKLEDGSLSRPQPEIEPEAAVQEMRPPTDLTHFKETQTH N+
Sbjct: 655 EEEEEKEEHEKKKKLEDGSLSRPQPEIEPEAAVQEMRPPTDLTHFKETQTHNM 708

>gb|AAB88191.1| (AF035526) kanadaptin [Mus musculus]
Length = 507

Score = 768 bits (1962), Expect = 0.0
Identities = 384/444 (86%), Positives = 411/444 (92%), Gaps = 1/444 (0%)

Query: 209 VRFGGSTRLFILQGPEEDREAESSELTVTQLKELRKQQQIILLXKKMLGEDSDEEEEMDTSE 268
+RFGGSTRLFILQGPEEDREAESSELTVTQLKELRKQQQIILLXKKMLGEDSDEEE +T+E
Sbjct: 1 MRFGGSTRLFILQGPEEDREAESSELTVTQLKELRKQQQIILLXKKMLGEDSDEEEANTTE 60

Query: 269 RKINAGSQDDEMGTWGMGEDAVEDDAEENPIVLEFQQEREAFYIKDPKKALQGFFDREG 328
K + QDDE+GCTWGMGEDAVED+AEENPI L+FQQ+REAFYIKDPKKALQGFFDREG
Sbjct: 61 GKSSRSQDDELGCTWGMGEDAVEDAEENPIALDFQQDREAFYIKDPKKALQGFFDREG 120

Query: 329 EELEYEFDEQGHSTWLCRVRLPVDDSTGKQLVAEAIHSGKKKEAMIQCSLEACRILDTLG 388
 EEELEYEFDEQGHSTWLCRVRLPVDDSTGKQLVAEAIHSGKKKEAM+QCSLEACR+LDTLG
 Sbjct: 121 EEELEYEFDEQGHSTWLCRVRLPVDDSTGKQLVAEAIHSGKKKEAMVQCSLEACRVLDTLG 180

Query: 389 LLRQEAVSRKRKAKNWEDEDFYDSDDDTFLDRTGLIEKKRLNRMKKAGKIDEKPETFESL 448
 LLRQEAVSRKRKAKNWEDEDFYDSDDDTFLDRTGL+EKKRLNRMKKAGK+DEKPETFESL
 Sbjct: 181 LLRQEAVSRKRKAKNWEDEDFYDSDDDTFLDRTGLVEKKRLNRMKKAGKLDEKPETFESL 240

Query: 449 VAKLNDARELSEISERLKASSQVLSESPSQDSLDAFMSEMKGSTLDGVSRRKKLHLRTF 508
 VAKLNDAREL+EISERLKASS+VLSE SQDSLDAFMSEMKGSTLDGVSRRKKLHLRTF
 Sbjct: 241 VAKLNDARELAEISERLKASSKVLSESPSQDSLDAFMSEMKGSTLDGVSRRKKLHLRTF 300

Query: 509 ELRKEQQRLKGLIKIVKPAEIPELKKTETQTTGAENKAKKLTLPFGAMKGGSKFKLKTG 568
 ELRKEQQRLKGLIK+VKPAEIPELKKTETQTT AENK KKL LPLFGAMKGGSKFKLKTG
 Sbjct: 301 ELRKEQQRLKGLIKLVKPAEIPELKKTETQTTAENKTKKLALPLFGAMKGGSKFKLKTG 360

Query: 569 TVGKLPPKRPELPPPTLMRMKDEPEV-EEEEEEEEEEEEKEKEEHEKKKLEDGSLSRPQPEI 627
 TVGKLPPKRPELPP LM+MKDEPEV EEEEEEEEEEEK KEEHE++ + G +PE+
 Sbjct: 361 TVGKLPPKRPELPPALMQMKDEPEVEEEEEEEEEEEKVKEEHEERVEDGGVRLQLPEL 420

Query: 628 EPEAAVQEMRPPTDLTHFKETQTH 651
 E EAAV+ P++ + KET++H
 Sbjct: 421 ELEAAVEHPSAPSEPSCKETKSH 444

>gb|AAF55582.1| (AE003723) CG7706 gene product [Drosophila melanogaster]
 Length = 726

Score = 337 bits (855), Expect = 2e-91
 Identities = 230/643 (35%), Positives = 323/643 (49%), Gaps = 82/643 (12%)

Query: 43 PEEVQKEGPTALQDSNSGEPDIPPPQPCDGRSLQEEQSRPTTAVSSPGGPAPAPPYQE 102
 P + K + S P PPP P P T SSP A PY+
 Sbjct: 7 PAPLPKPKVIIITEKPRSEVPAEPPPPP-----LKIPKTPKSSP---AAVCPYKV 52

Query: 103 PPWGGPATAP--YSLETLKGGTILGT-RSLKGTSYCLFGRLSGCDVCLHPSVSRYHAVL 159
 P W P YS E LK G I+ T L+ + FGRL DV HP++SR+H VL
 Sbjct: 53 PKWSAPPAENQIYSFEVLKSGQIIDTVHQLQQQAVWTFGRLPENDVPAAHPTISRHFVVL 112

Query: 160 QHRASGP-----DGECDNNGP-GFYLYDLGSTHGTFLNKTRIPPRTYCRV 203
 Q++ P D E ++ P G+Y+YD+GSTHGTFLNK R+PP+ Y R+
 Sbjct: 113 QYKPKAPPKPETAKEDDEMEEDDEEPKNDQPEGWYIYDMGSTHGTFLNKQRVPPKVYIRM 172

Query: 204 HVGHVVRFGGSTRLFILQGPEDREAESLTVTQLKELRKQQQILLXKKMLGEDSDDEEEE 263
 VGH+++ GGSTR++ILQGP ED E ESEL+VT+L++ R+++ D+ E E
 Sbjct: 173 RVGHMLKLGGSTRVYILQGPGEDEEPESELSVTELKQKREKEL-----ADAAVERE 223

Query: 264 MDTSERKINAGSQDDEMGCTWGMGEDAVED-DAENPIVLEFQQEREAFYIKDPKKALQG 322
 + R + A ++ G +WGMG+DA E+ D NP E + DPKK L+G
 Sbjct: 224 L----RLLEAEERERNEGVSWMGDDADEETDLSHNPYA---STNNEELFFDDPKKTLRG 276

Query: 323 FFDREGELEELEYEFDEQGHSTWLCRVRLPVDDSTGKQLVAEAIHSGKKKEAMIQCSLEACR 382
 FF+REG LEY+ DE +++CRV LP+DDS G+ ++ E H G+KK+ ++QC+LEACR
 Sbjct: 277 FFEREGLNLEYKCDDELSTGSFVCRVELPLDDSNRPRIIVEVNHKGRKKDCVVCALACR 336

Query: 383 ILDTLGLLRQ-EAVSRKRKAKNWEDEDFYDSDDDTFLDRTGLIEKKRLNRMKKAGKIDEK 441
 LD G+LRQ ++KRK D D D+D F DRTG + +K+ R AG
 Sbjct: 337 TLDRHGVLRQANQEAQKRKQLKNRDS-----DEDEFWDRTGDVARKK-QRKDNAGV--SV 389

Query: 442 PETFESLVAKLNDARELSEISERLKASSQ-----VLSESPSQDSLDAFMSEM-KSG 492
 T+E L+ + D E+ ++ + + Q + D LD FM + K
 Sbjct: 390 TLTYEDLLKQEIIDLNMEMEKVEQEISTYQQNEKKLKELAQQAEGDDLDFMDMLTKDV 449

Query: 493 STLDGVSRRKKLHLRTFELRKEQQRLKGLIKIVKPAEIP-----ELKKTETQTTGAENK 545
 LD KKL L ++ EQQ+++ L+KI KP +P K++ Q GA

Sbjct: 450 EQLDKTEIKKLRLEQQRIKGEQQKVERLLKIAKPTALPFTTSLAAGSKESAAQEGGA--- 506

Query: 546 AKKLTLPFLFGAMKGGSKFKLKTGTVGKLPPKRPELPPTLMRMKDEPEVEEEEEEEEEEEEEK 605
 AKK LP+ G SKFK V K P + + DE EEEEE +E+ +EK

Sbjct: 507 AKKKQLPMIGKRNFQFSKFK-----VVKASPSTQTMQSNAFASDEEEVEEEVEKEKVKKEK 561

Query: 606 EKEEHEKKKLEDGSLSRPQPEIEPEAAVQEMRPPTDLTHFKET 648
 E E +K E S +P +++E + P K T

Sbjct: 562 EAEVDNLEKEETEPESTTKPSTPENDSLKETKLPAQPEESKPT 604

>sp|P34648|YOT2 CAEEL HYPOTHETICAL 80.5 KD PROTEIN ZK632.2 IN CHROMOSOME III
 pir||S40934 hypothetical protein ZK632.2 - Caenorhabditis elegans
 emb|CAA80179.1| (Z22181) similar to Coiled coil protein~cDNA EST yk19b3.5 comes
 from this gene~cDNA EST yk231h11.3 comes from this
 gene~cDNA EST yk231h11.5 comes from this gene~cDNA EST
 yk418c1.3 comes from this gene~cDNA EST yk418c1.5 comes
 from this gene~cDNA EST yk>
 Length = 710

Score = 293 bits (741), Expect = 5e-78
 Identities = 217/649 (33%), Positives = 328/649 (50%), Gaps = 80/649 (12%)

Query: 18 GDFKKPALPVSPAARSKAPASSSSNPEEVQKEGPTALQDSNSGEPDIPPPQPCGDFRSL 77
 G FK P+LP P+ + AP S PE+++ P D P D

Sbjct: 6 GAFKSPSLP--PSHHAPAPMS----PEKIR--APAEQMDG-----PVEGVIDEIET 48

Query: 78 QEEQSRPTTAVSSPGGPARAPPYQEPWPW---GPATAPYSLETCLKGGTILGTRSL---KG 131
 E Q+ + +S A A Y+ PPW PA + E LK G ++ + L K

Sbjct: 49 AEVQAEKESKISVQ---APALHYEVPPWACEPDPAHK-FQFEILKEGKLIASYDLSNRKN 104

Query: 132 TSYCLFGRSL-GCDVLCLEHPSVSRYHAVLQHRASGPDGECDSNGPGFYLYDLGSTHGTFL 190
 +++ + GR+ GCD+ +EHP+SRYP +LQ+ G D + G G+++++LGSTHG+ +

Sbjct: 105 STFVVIGRIKPGCDLLMEHPSISRYHCILQY---GND-KMSKTGKGWHIFELGSTHGSRM 160

Query: 191 NKTRIPPRTYCRVHVGHVVRFGGSTRFLFIQGPPEEDREAESLTVTQLKELRKQQQILLX 250
 NK R+PP+ Y R VG + +FG STR+ GPEED E E + + T++K LRK ++ L

Sbjct: 161 NKKRLPPKQYIRTRVGFIQFGESTRILNFVGPPEEDSEPEWDCSPTMK-LRKHKKELEA 219

Query: 251 KKMLGEDSDDEEEMDTSERKINAGSQDDEMGTWGM--GED-----AVEDDAENPIVLE 303
 K +EM E++ + +E GC WGM GED VE DA

Sbjct: 220 KLRAAA----AQEMIDDEKR-----EKEEEGCGWGM DYGEDEKPLTTVETDAH----- 263

Query: 304 FQQEREAFYIKDPKKALQGFFDREGEELEYEFDEQGHs---TWLCRVRLPVD-DSTGKQL 359
 ++REA+Y +DPKKALQ FF+REG ++ +EF EQG W+C + LPV+ D +

Sbjct: 264 LMEDREAYYNQDPKKALQKFFEREGFDMNFEFSEQGQGHTHKWVCSIELPVEIDGVDRF 323

Query: 360 VAEAIHSGKKKEAMIQCSLEACRILDTLGLLRQEA VSRKRKAKNWEDEDFYDSDDDTFLD 419
 A A S KK+A IQC+L+ACRILDT +LR+ + + K E D+YD DDD +LD

Sbjct: 324 TASATVSTSKKDAQIQCALDACRILDTYNVLRKSNTKLRMQRKTL EANDYYDEDDDL YLD 383

Query: 420 RTGLIEKKRLNRMKKA---GKIDEKPFESLVAKLND AERELSEISERLKASSQVLSE 475
 RTG +EK+R R + A G + +T+ESL KL ++++E+ E + L S +

Sbjct: 384 RTGQLEKQREKRKQWAEEGFGHKRTETDTYESLCRKLEESKKEIIECQKHLDELSAGTKK 443

Query: 476 SPSQDS----LDAFMSEM-KSGSTLDGVSrk---KLHLRTFELRKEQQRLKGLIKIVKP 526
 S + D LD ++ ++ KSG D K K + E Q+L+ L+KI KP

Sbjct: 444 SRTIDQGGDVLDDYIRQLEKSGGAGDDAKTKMEKSKWRQKLMAATHESQKLEKLVKIAKP 503

Query: 527 AEIPELKKTTETQTTGAENKAKKLTLPFLFGAMKGGSKFKLKTGTVGKLPPKRPELPPTLMR 586
 A + L++ ET A N + L G K +T + G P LP T+

Sbjct: 504 AVVKGLEQLETT---AANDRQAFLLKLMGVR--ARKEIDQTPSQGPGPSTSATLPATV-- 556

Query: 587 MKDEPEVEEEEEEEEEEEKEEHEKKKLEDGSLSRPQPEIEPEAAVQE 635
 + E E E++ + E+ L+ + P ++ ++V++

Sbjct: 557 APTSTKAVEVEHEKKMTPLKVEKEIAASLDSSEIKNSLPVDEPSSVKD 605

>dbj|BAB08640.1| (AB009048) gene_id:K15E6.5~unknown protein [Arabidopsis thaliana]
Length = 729

Score = 189 bits (476), Expect = 6e-47

Identities = 180/663 (27%), Positives = 291/663 (43%), Gaps = 85/663 (12%)

Query: 27 VSPAARSKAPASSSSNPPEEVQKEGPTALQDSNSGEPDIPPP--QPDCGDFRSLQE----- 79
++ +A P + S+ E + T++ S+ PPP P+ D ++ +
Sbjct: 1 MTTSAMDP PPPRNP SHDIEPPEPNST SISQSD ETSTMNPPPPRNP NPPDLKTTEVVVEPE 60

Query: 80 --EQSRPTTAVSSPGGPAPARP-----PYQEPPWGGPATAPYSLET LKGGTILGTRSLK 130
E+S+ + P R PY P W GP + LE LK G I+ +
Sbjct: 61 PIEESKDDSVTVADAKPVRPRTVKQNPVPYTIPEWSGPPCHQFQLEVLKEGAIVEKLDVY 120

Query: 131 GTSYCLFGR LSGCDVCLHPSVSRYHAVLQHRASGPDGECDSNGPGFYLYDLGSTHGTFL 190
LFGR CD LEHPS+SR+HAV+Q++ SG Y++DLGSTHGT +
Sbjct: 121 KKGAYLFG RDGICDFALEHPSISRFAVIQYKRS G-----AAYIFDLGSTHGT TV 170

Query: 191 NKTRIPPRTYCRVHVGHVVRFGGSTRLFI LQGPEEDREA ESELTVTQLKELRKQQQILLX 250
NK ++ + + ++VG V+RFGGSTRL+I QGP + E +L Q++
Sbjct: 171 NKNKVDKKVFVDLNVGDVIRFGGSTRLYIFQGPSDLMPPEKDL-----QLIRE 218

Query: 251 KKMLGEDSD EEEEEMDT SERKINAGSQDDEMGTWGMGEDA VEDDAEENPIVL--EFQQR 308
KM E S+ E + + ++ + G +WGMGEDA+E++ ++ + + E
Sbjct: 219 AKMRMEMSEREASLR RARQQASMA D-----GVSWG MGEDAIEEEE DVEEITWQ TYSGEL 273

Query: 309 EAFYIKDPKKALQ-----GFFDREGEELEYEFDEQGHSTWLCRVRLPVDDSTGKQLVAEA 363
K +K L+ G +E + + QG T + ++ + +Q AE
Sbjct: 274 TPKQEKTK EKVLRLEKIGHMKKEVA AIRAKDISQGGLTQGGQTQI----ARNEQRTAEL 329

Query: 364 IHSGKKKEAMIQCSLEACRILDTLGLLRQEAVSRKRKA KNWEDEDFYDSDDDTFLDRTGL 423
+ + E + S I ++LG + +K EDE+ SD+D F DRT
Sbjct: 330 LEELENLEETLND S-----IRESLGAKTGRKPTHGKKKGIVEDEEDLSSDEDDFYDRT-- 382

Query: 424 IEKKRLNRMKKAGKIDEK PETFESLVAKLNDAERELSE-----ISERLKASSQVLSESPS 478
+KK K G ++ ET +SLV K ++ +E+ ++E+ K ++ ++E S
Sbjct: 383 -QKK---PSTKKGSENQT VETVDSLVDKRDNLKEIEAKNEQLL TEKSKMETENVTEVTS 438

Query: 479 QDS---LDAFMSEMKSGSTLDGVSRRKKLHLRTFELRKEQQRLKGLIKIVKPAEIP ELKKT 535
DS LDA+M+ + + D ++ + L T L+ E R+ L+KI P E+KK
Sbjct: 439 GDSL DALDAYMTGLSTTLVQDKTA IQQELST--LQSELSRILYLLKIADPTG-EEVKKR 495

Query: 536 ETQTTGAENKAKKLTLP LFGAMKGGSKFKLKTGT V GKLPKRPELPPTLMRMKDEPEVEE 595
E ++ E K KK P K + K E+ L+ +++PEVE
Sbjct: 496 ELKS--QELKIKKSETP-----SVEKKINIPLKQADPN EHKEKEVAKDLVDSENKPEVEN 548

Query: 596 EEEEEEEEEKEKEEHEKKLEDGSLSRPQ--PEIEPEAAVQEMRPPTDLTHFKETQTHGN 653
+ E EE+K K GS + E PE D F + + N
Sbjct: 549 KASETAEKKTTVYVPSKPQWL GSAANKAII EKNPEIVAATTDSTEDADGFVDYKNRKN 608

Query: 654 IFL 656
I L
Sbjct: 609 IAL 611

>pir||I51116 NF-180 - sea lamprey
gb|AAA80106.1| (U19361) NF-180 [Petromyzon marinus]
Length = 1110

Score = 72.2 bits (174), Expect = 2e-11

Identities = 101/440 (22%), Positives = 175/440 (38%), Gaps = 42/440 (9%)

Query: 225 EDREA ESELTVTQLKELRKQQQILLXKKMLGEDSD EEEEEMDTSE-RKINAGSQDDEMGT 283
E EAE+E T + E ++ + + GE+++E EE++ K A E+
Sbjct: 537 EVEEAEAEETEAEAA EEEEEAE GEEEAEEAEVEEEAIEKAEAAEAKAEVEEE 596

Query: 284 WGMGEDAVEDDAENPIVLEFQQEREAFYIKDPKKALQGFFDREGELEEYEFDEQ-GHST 342
 E+ E++AEE + E ++E EA + + EGE E E +E+
 Sbjct: 597 EAAEEEEEEEEEEVEAETKEEVEA-----EAEVEEEGEAAEEEEEEEEAE 646

Query: 343 WLCRVRLPVDSTGKQLVAEAIHSGKKKEAMIQCSLEACRILDTLGLLRQEAVSRKRKAK 402
 + + ++ ++ AEA + ++EA + E D ++E ++A
 Sbjct: 647 EVTSKKAKTQEAEEVEEEEAEEAEAEAEAEAEAEAGEE-----DVEAESKEEEEDSKEAD 701

Query: 403 NWEDEDFYDSDDDTFLDRTGLIEKKRLNRMKKAGKIDEKPEFESLVAKLND AEREL--- 459
 EDE + + + ++ E+ ++A K +E+ A+ +AE E
 Sbjct: 702 AEDEAEEEEVKEEEVTKSDA-EEAEAEAEAEAAKSEEEAAEEAKDEAEAEAEAEAEAVEE 760

Query: 460 ----SEISERLKASSQVLSESPSQDSLDAFMSEMKGSTLDGVSRRKKLHLRTF----- 508
 +E +E +AS E ++S E K +KK +
 Sbjct: 761 TEAATEEAEEAKEASDDEKPEEEVKESEAPVAPEAKKAPEPKAAPKKKAPAKVESPTSEPE 820

Query: 509 -ELRKEQQRLKGLIKIVKPAEIPELKKTETQTTGAENKAKKLT---PLFGAMKGGSKFK 564
 E + E KG + KP P K E + E + ++ P A +K
 Sbjct: 821 DEPKAEVVEKKGAEAPKPKAKPAAKKEAKPVEKEEEPEESPTTEEPKKPAAKPAKAP 880

Query: 565 LKTGTGKLPKRPELPPTLMRMKDEPEVEEEEEEEEEEEKEEHEKKKLEDGS--LSR 622
 K K + P + K P EEEE+E++E++E+EE E+ K ED S+
 Sbjct: 881 AKPKPAPKAEAEKPEPAKPAQAKPAPAAEEEEDEKEDDEEEEEEVEEVKPEDAKPVKSK 940

Query: 623 PQP----EIEPEAAVQEMRP 638
 P P E EP+ A Q +P
 Sbjct: 941 PAPAKEEEDPKPAKQPPKP 960

Score = 51.2 bits (120), Expect = 4e-05

Identities = 86/428 (20%), Positives = 164/428 (38%), Gaps = 62/428 (14%)

Query: 236 TQLKELRKQQQILLXKK--MLGEDSDEEEEMDTSERKINAGSQDDMGCTWGM--GEDAV 291
 T L++L Q++++ K ++ + DEEEE + E++ ++E G GE
 Sbjct: 462 TDLEDLA-QEEVMEAKAAPVVSAAEKDEEEEEEEEEEEKEEEAEAEAEAEEDRGRKEGEAEA 520

Query: 292 EDDAENPIVLEFQQEREAFYIKDPKKALQGFFDREGELEEYEFDEQGHSTWLCRVRLPV 351
 E++AEE + E +E E + + + + E E E E + +G
 Sbjct: 521 EEEAEAE-VEKEEAEEAEVEEAEEAEETEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAE 568

Query: 352 DDSTGKQLVAEAIHSGKKKEAMIQCSLEACRILDTLGLLRQEAVSRKRKAKNWEDEDFYD 411
 + +++ EAI + EA + +EA + + + + E+E+ +
 Sbjct: 569 EAEAEAEVEEEAEIAEAEAEAEAEVE-----EAEAEAEAEAEAEAEAEAEAEAEAEAEAE 614

Query: 412 SDDDTFLDRTGLIEKKRLNRMKKAGKIDEKPEFESLVAKLND AERELSEISERLKASSQ 471
 ++ ++ +E++ ++A + + + E S AK +AE E E + +
 Sbjct: 615 AETKEEVEAEAEVEEEGEAAEEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAEAE 674

Query: 472 VLSESPSQDSLDAFMSEMKGSTLDGVSRRK-----KLHLRTFELRKEQQRL 517
 E ++ ++A E + + + + + K E E++
 Sbjct: 675 EAEAEAGEEDVEAESKEEEEDSKEADAEEDEAEAEAEAEAEAEAEAEAEAEAEAEAEAE 734

Query: 518 KGLIKIVKPA-----EIPELKKTETQTTGAENKAKKLTPLFGAMKGGSKFKLKTGTV 570
 K + + A E E ET+ E +AK+ + K + K V
 Sbjct: 735 KSEEEAAEEAKDEAE 790

Query: 571 GKLPPKRPELPPTLMRMKDEPEVEEEEEEEEEEEKEEHEKKKLEDGSLSRPQPEIEPE 630
 K PE P K P E E E+E + E EKK G P+P+ +P
 Sbjct: 791 APEAKKAPE--PKAAPKKKAPAKVESPTSEPEDEPKAEVVEKK----GKAEAPKPKAKPA 844

Query: 631 AAVQEMRP 638
 AA +E +P
 Sbjct: 845 AAKKEAKP 852

Score = 49.2 bits (115), Expect = 1e-04

Identities = 57/232 (24%), Positives = 96/232 (40%), Gaps = 33/232 (14%)

Query: 436 GKIDEKPFESLVAKLND AERELSEISERLKASSQVLSE-SPSQDSLDAFMSEMKS--- 491
GK + E E + A+ E++E +L+ L + +++SL+ +SEM+
Sbjct: 296 GKFSQLTEAAEQNNDAIRSAKEEITEHRRKLQMRCTELDALAGTKESLERQLSEMEERHQ 355

Query: 492 ---GSTLDGVSRRKKLHLRT--FELRKEQQRLKGLIKIVKPAEIPELKKTETQTTGAENKA 546
G+ D + + LR +E+ + + L+ + +I E+ G E +
Sbjct: 356 SDVGNLQDAAQOLENELRNTKWEMARHLREYQDLLNVKMALDI-EIAAYRKLLDGEEIRY 414

Query: 547 KKLTLPLFGAMKGGSKFKLKTGTVGK-LPPKRPELP-----PTLMR 586
LP K K V K + K+PE+ +M
Sbjct: 415 SSGPLPTPAKPPKAPSAPKAAKVEKKVVSCKPEIKVESEPISAQLDTDLEDLAQEEVME 474

Query: 587 MKDEPEV---EEEEEEEEEEEEKEKEEHEKKKLEDGSLSRPQPEIEPEAAVQE 635
K P V ++EEEEEEEEEEKE+EE E ++ E+ R + E E E +E
Sbjct: 475 AKAAPVVSAAEKDEEEEEEEEEEEKEEEAAEEEEEDRGRKEGEAAEEEEAAE 526

Score = 34.8 bits (78), Expect = 3.0
Identities = 21/71 (29%), Positives = 35/71 (48%)

Query: 576 KRPELPPTLMRMKDEPEVEEEEEEEEEEEEEKEKEEHEKKKLEDGSLSRPQPEIEPEAAVQE 635
++ E +++E EEEEEEE EE+E E K+++E + + E E A +E
Sbjct: 582 EKAAEAAEAAEVEEEEEAAEEEEEEEEEEVEAETKEEVEAAEVEEEEGEAAEEEEAAE 641

Query: 636 MRPPTDLTHFK 646
++T K
Sbjct: 642 EAEVEEVTSSK 652

>gb|AAF45312.1| (AE002936) CG17168 gene product [Drosophila melanogaster]
Length = 421

Score = 71.8 bits (173), Expect = 2e-11
Identities = 49/134 (36%), Positives = 69/134 (50%), Gaps = 5/134 (3%)

Query: 100 YQEPWPWGGPATAPYSLET LKGGTILGTRSLKGTSYCLFGR-LSGCDVCLEHPSVSR YHAV 158
Y EPP + L KG T L T + S L GR D+ ++HPS S+ HA
Sbjct: 268 YSEPPEARKPKRRWRLYPFKGETALPTLHIHQSCFLVGRDRKVVLDLAVDHPSCSKQHAA 327

Query: 159 LQHRASGPDGECDSNGPG--FYLYDLGSTHGTFNLKTRIPRTYCRVHVGHVVRFGGSTR 216
LQ+R + E S+G YL DL S +GTFLN +I R Y + V++FG S+R
Sbjct: 328 LQYRLVPFEREDGSHGKRVRLYLIDLDSANGTFLNNKKIDARKYYELIEKDVIKFGFSSR 387

Query: 217 LFIL--QGPEEDRE 228
++L + +ED+E
Sbjct: 388 EYVLLHENSKEDE 401

>dbj|BAB11326.1| (AB016886) gene_id:MCA23.11~unknown protein [Arabidopsis thaliana]
Length = 369

Score = 69.1 bits (166), Expect = 1e-10
Identities = 45/128 (35%), Positives = 62/128 (48%), Gaps = 13/128 (10%)

Query: 100 YQEPWPW-GPATAPYSLET LKGGTILGTRSLKGTSYCLFGRL-SGCDVCLEHPSVSR YHA 157
+ P W P YSLE +K G IL L + +FGR CD L+H SVSR HA
Sbjct: 52 WHPPDWAIEPRAGVYSLEVVKDQILDRIHLDRRRH-IFGRQHQTCDVLDHQSVSRQHA 110

Query: 158 VLQHRASGPDGECDSNGPGFYLYDLGSTHGTFNLKTRIPRTYCRVHVGHVVRFGGSTRL 217
+ +G ++ DLGS HGTF+ R+ T + VG +RF STR+
Sbjct: 111 AVVPHKNG-----SIFVIDLGSAGHTFVANERLT KDTPVELEVQSLRFAASTRI 160

Query: 218 FILQGPEE 225
++L+ E
Sbjct: 161 YLLRKNSE 168

>pir||T25596 hypothetical protein C32E8.5 - Caenorhabditis elegans
gb|AAB42323.1| (U88308) C32E8.5 gene product [Caenorhabditis elegans]
Length = 299

Score = 67.5 bits (162), Expect = 4e-10
Identities = 56/197 (28%), Positives = 90/197 (45%), Gaps = 18/197 (9%)

Query: 43 PEEVQKEGPT---ALQDSNSGEPDIPPPQPD---CGDFRSLQEEQSRPTTAVSSPGGPAR 96
P+ V+++G ++ N G+P+ P + + G +L E+ + V
Sbjct: 99 PDPVREDGKQYGLEKKEENWGWKPEEPAKEKEKVNLTSGALTEDTNTFRGVVIK----- 152

Query: 97 APPYQEPWPWGGPATAPYSLETLKGGTILGTRSLKGTSYCLFGRLSG-CDVCLEHPSVSRY 155
Y EPP A + L KG L + S L GR D+ ++HPS S+
Sbjct: 153 ---YNEPPEAKKPNARWRLYPFKGEESLQVLYIHRQSAYLIGRDHKIADIPVDHPSCSKQ 209

Query: 156 HAVLQHRASGPDGECDSNGPGF--YLYDLGSTHGTFLNKTRIPRTYCRVHVGHVVRFGG 213
HAVLQ R+ + + Y+ DLGS +GTFLN+ +I P+ Y + +++FG
Sbjct: 210 HAVLQFRSMFPTRDDGTKARRIMPYIIDLGSGNGTFLNEKKIEPQRYIELQEKDMLKFGF 269

Query: 214 STRLFILQGPPEEDREAE 230
STR +++ E E E
Sbjct: 270 STREYVVMKEREITEEE 286

>sp|Q28147|PPR8 BOVIN NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 (NIPP-1) (PROTEIN
PHOSPHATASE 1, REGULATORY INHIBITOR SUBUNIT 8)
pir||I46033 NIPP-1, nuclear inhibitor of protein phosphatase-1 - bovine
emb|CAA90625.1| (Z50748) NIPP-1, nuclear inhibitor of protein phosphatase-1 [Bos
taurus]
Length = 351

Score = 66.0 bits (158), Expect = 1e-09
Identities = 40/125 (32%), Positives = 57/125 (45%), Gaps = 10/125 (8%)

Query: 98 PPYQEPWPWGGPATAPYSLETLKGGTILGTRSLKGTSYCLFGRLSG-CDVCLEHPSVSRYH 156
P + P W G L+ +KG ++ + Y LFGR CD ++H S SR H
Sbjct: 12 PLFDCPTWAGKPPPGLHLDVVKGDKLIIEKKYYLFGRNPDLCDFTIDHQSCSRVH 71

Query: 157 AVLQHRASGPDGECDSNGPGFYLYDLGSTHGTFLNKTRIPRTYCRVHVGHVVRFGGSTR 216
A L + + +L DL STHGTF L R+ P ++ + V FG STR
Sbjct: 72 AALVYH-----KHLKRVFLIDLNSTHGTF LGHIRLEPHKPPQIPIDSTVSFGASTR 122

Query: 217 LFILQ 221
+ L+
Sbjct: 123 AYTLR 127

Database: nr
Posted date: Oct 24, 2000 1:47 AM
Number of letters in database: 181,542,687
Number of sequences in database: 576,719

Lambda	K	H
0.310	0.131	0.373

Gapped Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 262444375
Number of Sequences: 576719
Number of extensions: 13092420
Number of successful extensions: 184874
Number of sequences better than 10.0: 2439

Number of HSP's better than 10.0 without gapping: 1108
Number of HSP's successfully gapped in prelim test: 1433
Number of HSP's that attempted gapping in prelim test: 126441
Number of HSP's gapped (non-prelim): 20962
length of query: 667
length of database: 181,542,687
effective HSP length: 61
effective length of query: 606
effective length of database: 146,362,828
effective search space: 88695873768
effective search space used: 88695873768
T: 11
A: 40
X1: 16 (7.2 bits)
X2: 38 (14.8 bits)
X3: 64 (24.9 bits)
S1: 42 (21.7 bits)
S2: 74 (33.2 bits)